RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/803,459C_

Source: _1FWO,_

Date Processed by STIC: _1/14/05_

ENTERED

IFWO

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RAW SEQUENCE LISTING                         DATE: 01/14/2005
PATENT APPLICATION:   US/10/803,459C         TIME: 12:42:13

Input Set : D:\Leptin Sequence Listing-Corrected.3.txt
Output Set: N:\CRF4\01142005\J803459C.raw
```

```
       3 <110> APPLICANT: Gertler, Arieh
       4         Krishna, Radha G.
       6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO
       8 <130> FILE REFERENCE: 28758.1
C-->  10 <140> CURRENT APPLICATION NUMBER: US/10/803,459C
C-->  10 <141> CURRENT FILING DATE: 2004-03-19
      10 <160> NUMBER OF SEQ ID NOS: 8
      12 <170> SOFTWARE: PatentIn version 3.2
      14 <210> SEQ ID NO: 1
      15 <211> LENGTH: 630
      16 <212> TYPE: DNA
      17 <213> ORGANISM: homo sapiens
      20 <220> FEATURE:
      21 <221> NAME/KEY: CDS
      22 <222> LOCATION: (1)..(630)
      24 <220> FEATURE:
      25 <221> NAME/KEY: misc_feature
      26 <222> LOCATION: (6)..(6)
      27 <223> OTHER INFORMATION: n is a, c, g, or t
      29 <400> SEQUENCE: 1
W-->  30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac        48
      31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
      32 1               5                   10                  15
      34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt        96
      35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
      36             20                  25                  30
      38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt       144
      39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
      40         35                  40                  45
      42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat       192
      43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
      44     50                  55                  60
      46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta       240
      47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
      48 65                  70                  75                  80
      50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca       288
      51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
      52             85                  90                  95
      54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca       336
      55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
      56             100                 105                 110
      58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta       384
      59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
```

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Input Set : **D:\Leptin Sequence Listing-Corrected.3.txt**
Output Set: **N:\CRF4\01142005\J803459C.raw**

```
60         115                120                125
62 ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa      432
63 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
64      130                135                140
66 ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg      480
67 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
68 145                150          .      155                160
70 tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca      528
71 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
72             165                170                175
74 gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat      576
75 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
76          180                185                190
78 gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc      ·624
79 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
80          195                200                205
82 atg gat                                                              630
83 Met Asp
84      210
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 210
89 <212> TYPE: PRT
90 <213> ORGANISM: homo sapiens
92 <400> SEQUENCE: 2
94 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
95 1             5                10                15
98 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
99          20                25                30
102 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
103         35                40                45
106 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
107      50                55                60
110 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
111 65                70                75                80
114 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
115             85                90                95
118 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
119         100                105                110
122 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
123         115                120                125
126 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
127      130                135                140
130 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
131 145                150                155                160
134 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
135             165                170                175
138 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
139         180                185                190
142 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
```

```
143           195              200            205
146 Met Asp
147     210
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 36
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: completely synthesized
158 <400> SEQUENCE: 3
159 ggaattccat atgattgatg tcaatatcaa tatctc                           36
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 39
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: completely synthesized
170 <400> SEQUENCE: 4
171 cataggaagc tttcaatcca tgacaactgt gtaggctgg                        39
174 <210> SEQ ID NO: 5
175 <211> LENGTH: 12
176 <212> TYPE: PRT
177 <213> ORGANISM: homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: misc_feature
182 <222> LOCATION: (11)..(11)
183 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
185 <400> SEQUENCE: 5
W--> 187 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu
188 1             5                   10
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 5
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (3)..(3)
200 <223> OTHER INFORMATION: Consensus sequence, Xaa can be any naturally occurring amino
acid
202 <400> SEQUENCE: 6
W--> 204 Trp Ser Xaa Trp Ser
205 1             5
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 627
210 <212> TYPE: DNA
211 <213> ORGANISM: gallus domesticus
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (1)..(627)
218 <220> FEATURE:
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        219 <221> NAME/KEY: misc_feature
        220 <222> LOCATION: (6)..(6)
        221 <223> OTHER INFORMATION: n is a, c, g, or t
        223 <400> SEQUENCE: 7
W-->    224 atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac        48
        225 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
        226 1               5                   10                  15
        228 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc        96
        229 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
        230             20                  25                  30
        232 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt       144
        233 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
        234         35                  40                  45
        236 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat       192
        237 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
        238     50                  55                  60
        240 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt       240
        241 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
        242 65                  70                  75                  80
        244 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca       288
        245 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
        246                 85                  90                  95
        248 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca       336
        249 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
        250             100                 105                 110
        252 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg       384
        253 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
        254         115                 120                 125
        256 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag       432
        257 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
        258     130                 135                 140
        260 ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg       480
        261 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
        262 145                 150                 155                 160
        264 tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa       528
        265 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
        266                 165                 170                 175
        268 ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc       576
        269 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
        270             180                 185                 190
        272 tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa       624
        273 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
        274             195                 200                 205
        276 gat                                                                   627
        277 Asp
        281 <210> SEQ ID NO: 8
        282 <211> LENGTH: 209
        283 <212> TYPE: PRT
        284 <213> ORGANISM: gallus domesticus
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```
286 <400> SEQUENCE: 8
288 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
289 1               5                   10                  15
292 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
293             20                  25                  30
296 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
297         35                  40                  45
300 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
301     50                  55                  60
304 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
305 65                  70                  75                  80
308 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
309             85                  90                  95
312 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
313             100                 105                 110
316 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
317         115                 120                 125
320 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
321     130                 135                 140
324 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
325 145                 150                 155                 160
328 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
329             165                 170                 175
332 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
333             180                 185                 190
336 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
337         195                 200                 205
340 Asp
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/14/2005
PATENT APPLICATION: US/10/803,459C   TIME: 12:42:14

Input Set : **D:\Leptin Sequence Listing-Corrected.3.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6
Seq#:5; Xaa Pos. 11
Seq#:6; Xaa Pos. 3
Seq#:7; N Pos. 6

VERIFICATION SUMMARY   DATE: 01/14/2005
PATENT APPLICATION: US/10/803,459C   TIME: 12:42:14

Input Set : **D:\Leptin Sequence Listing-Corrected.3.txt**
Output Set: **N:\CRF4\01142005\J803459C.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0